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GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2001, 12:06:13 ; Search time 16.04 Seconds  
(without alignments)

Sequence: 1491.198 Million cell updates/sec

Title: US-09-486-334-2

Perfect score: 1641

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 68;\*

1: Pir1;\*  
2: Pir2;\*  
3: Pir3;\*  
4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1641	100.0	S67482	serine O-acetyltransferase (EC 2.3.1.30), cytosolic - <i>Arabidopsis thaliana</i>
2	1611	98.2	S71181	serine O-acetyltransferase
3	1215	74.0	S69192	serine O-acetyltransferase
4	1105	67.3	S68469	serine O-acetyltransferase
5	877	53.4	T09140	serine O-acetyltransferase
6	869	53.0	A57478	serine O-acetyltransferase
7	849.5	51.8	S71207	probable serine acetyltransferase
8	699	42.6	F84554	probable serine O-acetyltransferase
9	649.5	39.6	C81184	serine O-acetyltransferase
10	648.5	39.5	XIECSA	serine O-acetyltransferase
11	648.5	39.5	S29568	serine acetyltransferase
12	648.5	39.5	F86036	serine acetyltransferase
13	647.5	39.5	G82049	serine O-acetyltransferase
14	643	39.2	T08867	serine O-acetyltransferase
15	624.5	38.1	G64080	probable serine O-acetyltransferase
16	587.5	35.8	T04659	serine O-acetyltransferase
17	573.5	34.9	A84936	serine O-acetyltransferase
18	549.5	33.5	JC1293	probable serine acetyltransferase
19	472.5	28.8	T50058	serine O-acetyltransferase
20	442	26.9	E53402	serine O-acetyltransferase
21	424	25.8	B53402	probable serine O-acetyltransferase
22	422.5	25.7	T44913	serine O-acetyltransferase
23	420.5	25.6	S75605	serine O-acetyltransferase
24	405	24.9	T44279	probable serine acetyltransferase
25	405	24.7	H70660	serine O-acetyltransferase
26	395	24.1	F83663	O-acetylyserine synthase
27	392	23.9	A83169	serine O-acetyltransferase
28	389.5	23.7	E86856	serine O-acetyltransferase
29	387	23.7	C81347	serine O-acetyltransferase

srpH protein - Srp

probable acetyltransferase

probable acetyltransferase

serine acetyltransferase

acetyltransferase

serine acetyltransferase

2,3,4,5-tetrahydrodipicolyl hypothetical protein

tetrahydrodipicolyl nodulation protein

30 369.5 22.5 269 1 D43706  
31 355 22.2 171 1 B64671  
32 359 21.9 171 2 B71845  
33 338 20.6 220 2 G72349  
34 312 19.0 171 2 D84302  
35 287 17.5 319 2 S53322  
36 265 16.1 231 2 H83381  
37 217 13.2 162 2 A64972  
38 207 13.2 162 2 B88382  
39 207 12.6 184 2 C82264  
40 179 10.9 256 2 A86660  
41 177.5 10.8 143 2 G82264  
42 175 10.7 235 2 H72245  
43 175 10.7 240 2 E83806  
44 171 10.4 201 2 H85D06  
45 164.5 10.0 190 2 S07000

ALIGMENTS

30 369.5 22.5 269 1 serine O-acetyltransferase  
31 355 22.2 171 1 serine O-acetyltransferase  
32 359 21.9 171 2 o-serine acetyltransferase  
33 338 20.6 220 2 serine acetyltransferase  
34 312 19.0 171 2 srpH protein - Srp  
35 287 17.5 319 2 probable acetyltransferase  
36 265 16.1 231 2 probable acetyltransferase  
37 217 13.2 162 2 probable acetyltransferase  
38 207 13.2 162 2 serine acetyltransferase  
39 207 12.6 184 2 acetyltransferase  
40 179 10.9 256 2 serine acetyltransferase  
41 177.5 10.8 143 2 2,3,4,5-tetrahydrodipicolyl  
42 175 10.7 235 2 tetrahydrodipicolyl  
43 175 10.7 240 2 hypothetical protein  
44 171 10.4 201 2 nodulation protein  
45 164.5 10.0 190 2 S07000

RESULT 1

Query Match 100.0%; Score 1641; DB 314; Length 314;

Best Local Similarity 100.0%; Pred. No. 8.8e-129; Mismatches 0; Indels 0; Gaps 0;

Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATCIDTCRGNODDSRSFRCIKNFRPGPSVNRKIHHTQIEDDDWVKMPEAKSDV 60

Db 1 MATCIDTCRGNODDSRSFRCIKNFRPGPSVNRKIHHTQIEDDDWVKMPEAKSDV 60

QY 61 KQEPILSNYYASTISHSRSLAHILSVKLNSLNHPSPILTFELFISLESEPEIEST 120

Db 61 KQEPILSNYYASTISHSRSLAHILSVKLNSLNHPSPILTFELFISLESEPEIEST 120

QY 121 KQDLIAKVERDPACTSYWVCFGLFGKFLACQHRTAATLQKONRKVALLIONVSEFA 180

Db 121 KQDLIAKVERDPACTSYWVCFGLFGKFLACQHRTAATLQKONRKVALLIONVSEFA 180

QY 181 VDIHPSAKIGKGLIDHATGWVGETAVWGDNVSLHGVPJGGTGKQSGRHPKIGDGV 240

Db 181 VDIHPSAKIGKGLIDHATGWVGETAVWGDNVSLHGVPJGGTGKQSGRHPKIGDGV 240

QY 301 DOTSYLEWSIVVI 314

Db 301 DOTSYLEWSIVVI 314

RESULT 2

S71181

serine O-acetyltransferase (EC 2.3.1.30) SAT1 precursor, chloroplast - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 19-Aug-1997 #sequence\_revision 25-Apr-1997 #text\_change 05-May-2000  
 C;Accession: S71181  
 R;Murillo, M.; Foglia, R.; Diller, A.; Leustek, T.  
 submitted to the EMBL Data Library, August 1995  
 A;Description: Analysis of a cDNA encoding serine acetyltransferase from Arabidopsis thaliana of Escherichia coli  
 A;Reference number: S71181  
 A;Accession: S71181  
 A;Residues: 1-314 <MUR>  
 A;Cross-references: EMBL:L42212; NID:9926938; PIDN:AC37474.1; PID:9926939  
 A;Note: probably chloroplast isoform; no transit peptide given  
 C;Genetics:  
 A;Genome: nuclear  
 C;Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C;Keywords: acetyltransferase; chloroplast; coenzyme A; cysteine biosynthesis  
 C;Keywords: acetyltransferase; chloroplast; coenzyme A; cysteine biosynthesis  
 F;123-283/Domain: serine acetyltransferase homology <SAT>  
 Query Match 74.0%; Score 1215; DB 2; Length 391;  
 Best Local Similarity 98.2%; Score 1611; DB 2; Length 314;  
 Matches 308; Conservative 2; Mismatches 41; Indels 22; Gaps 4;  
 QY 1 MATCIDIQRTGNTQDDPSRECCKIKNFRPGFSYNRKTHIQTIEDDDWVWIKMLEAKSDV 60  
 1 MATCIDIQRTGNTQDDPSRECCKIKNFRPGFSYNRKTHIQTIEDDDWVWIKMLEAKSDV 60  
 Db 61 KOPILSNYYVYSITSRSLSAHLISKLNLPSNLPSNTLFLFISYLEEPTEEST 120  
 61 KOPILSNYYVYSITSRSLSAHLISKLNLPSNLPSNTLFLFISYLEEPTEEST 120  
 Db 121 KODLIAVKERPACTSYVHCELGKFLACQAHRLAHTWKONRIVALLIONRVSSFA 180  
 121 KODLIAVKERPACTSYVHCELGKFLACQAHRLAHTWKONRIVALLIONRVSSFA 180  
 Db 181 VDHPGAKIGKGILLDHATGVNIGETAVVGDNVSTLHGVTGLGGKGKSGDRHPKIGDGV 240  
 181 VDHPGAKIGKGILLDHATGVNIGETAVVGDNVSTLHGVTGLGGKGKSGDRHPKIGDGV 240  
 Qy 241 IGAGSCLGNITIGGAKIGGSVWVKDVPARTAVGMPARLIGKPNPKDKIPCLTM 300  
 241 IGAGSCLGNITIGGAKIGGSVWVKDVPARTAVGMPARLIGKPNPKDKIPCLTM 300  
 Db 301 DQTSTLLEWSDYVI 314  
 301 DQTSTLLEWSDYVI 314  
 Db 301 DQTSTLLEWSDYVI 314  
 RESULT 3  
 S69192  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Accession: 05-Dec-1995 #sequence\_revision 21-Feb-1997 #text\_change 05-May-2000  
 R;Roberts, M.A.; Wray, J.L.  
 Plant Mol. Biol. 30, 1041-1049, 1996  
 A;Title: Cloning and characterisation of an Arabidopsis thaliana cDNA clone encoding an  
 A;Reference number: S69192; MUID:96270381  
 A;Accession: S69192  
 A;Molecule type: mRNA  
 A;Residues: 1-391 <ROB>  
 A;Cross-references: EMBL:022964; NID:91184047; PIDN:AAB07778.1; PID:91184048  
 submitted to the EMBL Data Library, July 1995  
 A;Reference number: S71906  
 A;Accession: S71906  
 A;Molecule type: mRNA  
 A;Residues: 1-391 <HEL>  
 A;Cross-references: EMBL:X82888; NID:9897677; PIDN:CA58061.1; PID:9897678  
 C;Genetics:  
 A;Genome: nuclear

Query Match 74.0%; Score 1215; DB 2; Length 391;  
 Best Local Similarity 98.2%; Score 1611; DB 2; Length 314;  
 Matches 308; Conservative 2; Mismatches 41; Indels 22; Gaps 4;  
 QY 1 MATCIDIQRTGNTQDDPSRECCKIKNFRPGFSYNRKTHIQTIEDDDWVWIKMLEAKSDV 60  
 1 MATCIDIQRTGNTQDDPSRECCKIKNFRPGFSYNRKTHIQTIEDDDWVWIKMLEAKSDV 60  
 Db 56 MAACIDTGTGKPOISPRDSKHHDESFGFMYFVPRSSENGFTOKTILHTRPLLED 115  
 QY 45 -----DDDWVWIKMLEAKSDVQEPILSNYYASSTSHSLSELAHTLVSQNLNP 98  
 45 -----DDDWVWIKMLEAKSDVQEPILSNYYASSTSHSLSELAHTLVSQNLNP 98  
 Db 116 LDRDAEVDDWAKIREAKSDIAKEPIVSVYHASYISVQSLERALANTLSVKLSNLNP 175  
 QY 99 SNLFLFIFSVIEESPITEESTKODLIAVKERDFACTSYVHCELGKFLACOAHRAHT 158  
 99 SNLFLFIFSVIEESPITEESTKODLIAVKERDFACTSYVHCELGKFLACOAHRAHT 158  
 Db 176 SNLFLFIFSGVQLNQFDIVESVKLDLAVKERDFACTSYVHCELGKFLACOAHRAHT 235  
 QY 159 LNKONRKLVALIQLNQVSEFADVHDHPGAKIGKGILLDHATGVNIGETAVVGDNVSLHG 218  
 159 LNKONRKLVALIQLNQVSEFADVHDHPGAKIGKGILLDHATGVNIGETAVVGDNVSLHG 218  
 Db 236 LMTQDRKTLALLIONKVSEAFAVDFHPGAKIGKGILLDHATGVNIGETAVVGDNVSLHN 295  
 QY 219 VLGCGKGKOSDRHKIGDGVLWIGLIGASCILGNTIGEGAGSGSVVWVKDVPARTAVGN 278  
 219 VLGCGKGKOSDRHKIGDGVLWIGLIGASCILGNTIGEGAGSGSVVWVKDVPARTAVGN 278  
 Db 296 VLGCGKGKOSDRHKIGDGVLWIGLIGAGTCILGNTIGEGAGSGSVVWVKDVPARTAVGN 355  
 QY 279 PARLIGKKGKVERKHKIKPLTMOTOSLYTEWSDYVI 314  
 279 PARLIGKKGKVERKHKIKPLTMOTOSLYTEWSDYVI 314  
 Db 356 PARLIGKKGKVERKHKIKPLTMOTOSLYTEWSDYVI 39:  
 RESULT 4  
 S68469  
 C;Species: O-acetyltransferase (EC 2.3.1.30) sata - Arabidopsis thaliana  
 C;Accession: S68469  
 R;Bogdanova, N.; Bork, C.; Hell, R.  
 FEBS Lett. 358, 43-47, 1995  
 A;Title: Cysteine biosynthesis in plants: isolation and functional identification of  
 A;Reference number: S68469; MUID:95121457  
 A;Accession: S68469  
 A;Molecule type: mRNA  
 A;Residues: 1-303 <BOG>  
 C;Cross-references: EMBL:X82888  
 C;Genetics:  
 A;Gene: sata  
 C;Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C;Keywords: acetyltransferase; coenzyme A; cysteine biosynthesis  
 F;113-272/Domain: serine acetyltransferase homology <SAT>  
 Query Match 67.3%; Score 1105; DB 2; Length 303;  
 Best Local Similarity 73.0%; Score 1105; DB 2; Length 303;  
 Matches 222; Conservative 30; Mismatches 36; Indels 16; Gaps 6;  
 QY 25 NFPR-PGFS---VNRKTHIQT---IED-----DDDWVWIKMLEAKSDVQEPILSNYY 71  
 25 NFPR-PGFS---VNRKTHIQT---IED-----DDDWVWIKMLEAKSDVQEPILSNYY 71  
 Db 2 NYFRPDPRSSFNFGTQTKTHTRPLLEDLDRDAEVDDWAKIREAKSDIAKEPIVSVYH 61  
 QY 72 ASITSRSLSAHLISKLNLPSNLPSNTLFLFISYLEEPTEESTKODLIAVKERD 131  
 72 ASITSRSLSAHLISKLNLPSNLPSNTLFLFISYLEEPTEESTKODLIAVKERD 131  
 Db 62 ASIVSQRSYEALANTLSVKLSNLPSNTLFLFISYLEEPTEESTKODLIAVKERD 131  
 Qy 132 PACISVYHCELGKFLACOAHRLAHTWKONRIVALLIONRVSSFAVDIHPGAKIG 191  
 132 PACISVYHCELGKFLACOAHRLAHTWKONRIVALLIONRVSSFAVDIHPGAKIG 191



QY 288 NPXKHD-KIPCHLMDOTSYLNEWSDVI 314 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandren Nature 404, 502-506, 2000  
 Db 285 KTIHDBECPGESMDHTSFISSEWSDVII 312 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491  
 C;Accession: F84554 A;Reference number: A81775; MUID:2022556  
 RESULT 8 A;Status: Preliminary  
 F84554  
 probable serine acetyltransferase [imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C;Accession: F84554 A;Accession: H81917  
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Stien, M.; Vanaken, S.E.; Umaran, L.; Tailor, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A;Reference number: A84420; MUID:20083487  
 A;Accession: F84554 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Map position: 2  
 C;Genetics:  
 A;Cross-references: GB:AE002093; NID:96598796; PIDN:AAF18673.1; GSPDB:GN00139  
 A;Gene: CYSE; NMB0560; NMA0742  
 A;Experimental source: serogroup A, strain Z2491  
 C;Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C;Keywords: acetyltransferase; coenzyme A  
 F;88-248/Domain: serine acetyltransferase homology <SAT>  
 Query Match 42.6%; Score 699; DB 2; Length 315; Best Local Similarity 50.2%; Pred. No. 1. 6e-50; Matches 141; Conservative 50; Mismatches 76; Indels 14; Gaps 4; QY 27 FRGGFSVNRK-TIHTQTEDD----DDWIKMLERAKSDVKQEPILSNNYIASITSHRS 79 Db 8 FEGFEVYAKGTHKSEFDNLIDPDRSDPIMDAIREAK--LEKEPIILSSFLYACILANDC 65  
 QY 80 LEZALAHILSVKLNSNLPSNWLPEELFISLEESPELIESTIKOLIAVVERDPACISVH 139 Db 66 LFGALGVFLANRQLNPPTLATQQLDIFGYQAMHDKIQSSIRHQLQAFKRDPCALSISS 125  
 QY 140 CTFGEKFLAQAHRAHTLMQNKRKIVALLIONKVSESAFDTHPGAKIGKILLRHAT 199 Db 126 ATILHKYHALQAYRATAHKUNLQLAORSRISVEFGIDHTHPARIGEGILLDGT 185  
 QY 200 GVVIGETAVWDNVSLHAGVYGLGKGQSDRHKRKGDKGVLIGAGSCTIGNITIGEAKI 259 Db 186 GVVIGETAVIGNGVSILHGVLGKGKENGDRHKRKGEGALIGCVTILGNISGAGMV 245  
 QY 260 GSGSVVWKDVPARTAVGNPARLTGKPNRHKIIPCITM 300 Db 246 AAGSLVLUKDPSHWSVAGNPAAKLRVME----EQDPSLAM 281  
 RESULT 9  
 C81184 PROBABLE SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) NMA0742 [imported] - *Neisseria meningitidis* A;Accession: A27895; MUID:20175755  
 C;Species: *Neisseria meningitidis* C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 02-Feb-2001  
 C;Accession: C01184; H81917 R;Tettelein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Yamatobean, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000  
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Weisblum, B.; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel A;Reference number: A81000; MUID:20175755  
 A;Accession: C81184 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-272 <TET>  
 A;Cross-references: GB:AE002412; GB:AE002098; NID:97225783; PIDN:AAF40988.1; PID:9722578 A;Cross-references: serogroup B, strain MC58  
 A;Experimental source: serogroup B, strain MC58 R;Plunkett, G. A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58. A;Reference number: A81000; MUID:20175755  
 A;Accession: C81184 A;Accession: A27895; MUID:88009872  
 A;Molecule type: DNA  
 A;Residues: 1-273 <DEN>  
 A;Cross-references: GB:MA15745; MID:9145675; PIDN:AAA23648.1; PID:9145676 R;Tei, H.; Murata, K.; Kimura, A.  
 Biochem. Biophys. Res. Commun. 167, 948-955, 1990  
 A;Title: Structure and expression of the *Escherichia coli* K-  
 A;Reference number: A34563; MUID:90311342 A;Accession: A34563  
 A;Molecule type: DNA  
 A;Residues: 1-273 <TER>  
 A;Cross-references: GB:M34333; NID:9145693; PIDN:AAA23659.1; PID:9145694 R;Plunkett, G. A;Title: L-Cysteine biosynthesis in *Escherichia coli*: nucleotide sequence and express  
 A;Reference number: A27896; MUID:88009872  
 A;Accession: A27895  
 A;Molecule type: DNA  
 A;Residues: 1-273 <DEN>  
 A;Cross-references: GB:MA15745; MID:9145675; PIDN:AAA23648.1; PID:9145676 R;Tei, H.; Murata, K.; Kimura, A.  
 Biochem. Biophys. Res. Commun. 167, 948-955, 1990  
 A;Title: Structure and expression of the *Escherichia coli* K-  
 A;Reference number: A34563; MUID:90311342 A;Accession: A34563  
 A;Molecule type: DNA  
 A;Residues: 1-273 <PLU>  
 A;Cross-references: EMBL:U00039; NID:9466582; PIDN:AA818584.1; PID:9466745 R;Blattner, F.R.; Plunkett III, G.; Blech, C.A.; Perria, N.T.; Burland, V.; Riley, M.; A;Rose, D.J.; Mu, B.; Shao, Y.

Science 277, 1453-1462, 1997  
 A; Title: The complete genome sequence of Escherichia coli K-12.  
 A; Reference number: A64720; MUID:97426617  
 A; Accession: A65161  
 A; Molecule type: DNA  
 A; Residues: 1-273 <BLAT>  
 A; Cross-references: GB:AE000438; GB:U00096; NID:92367251; PIDN:AC76631.1; PID:gi1790035;  
 A; Experimental source: strain K-12, substrate MG1655  
 C; Comment: This enzyme catalyzes the conversion of L-serine to O-acetyl serine (by acetyl  
 A; Gene: cySE  
 A; Map position: 81 min  
 C; Superfamily: serine acetyltransferase; coenzyme A; cysteine biosynthesis  
 C; Keywords: aminoacyltransferase; coenzyme A; cysteine biosynthesis  
 F; 84-244/Domain: serine acetyltransferase homology <SAT>

Query Match 39.5%; Score 648.5; DB 1; Length 273;  
 Best Local Similarity 50.8%; Pred. No. 2e-46; Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;  
 C; Species: Escherichia coli  
 C; Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
 C; Accession: F8036  
 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apoda  
 Nature 409, 529-533, 2001  
 A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A; Reference number: A85480; MUID:21074935; PMID:11206551  
 A; Accession: F8036  
 A; Status: Preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-273 <STO>  
 A; Cross-references: GB:AE00514; NID:912518357; PIDN:AA58754.1; GSPDB:GN00145; UWGB:  
 A; Experimental source: strain O157:H7, substrate 1; M933  
 C; Genotype: cySE  
 C; Superfamily: serine acetyltransferase; serine acetyltransferase homology

Query Match 39.5%; Score 648.5; DB 2; Length 273;  
 Best Local Similarity 50.8%; Pred. No. 2e-46; Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;  
 C; Species: Salmonella typhimurium  
 C; Date: 22-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-May-2000  
 C; Accession: S29568  
 R; Srivaprabad, A.V.; Kuczek, E.S.; Bawden, C.S.; Rogers, G.E.  
 A; Submitted to the EMBL Data library, May 1991  
 A; Reference number: S29567  
 A; Accession: S29568  
 A; Molecule type: DNA  
 A; Residues: 1-273 <SIV>  
 A; Cross-references: EMBL:X59594; NID:947659; PIDN:CAA42163.1; PID:gi47660  
 C; Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C; Keywords: acyltransferase; coenzyme A  
 F; 84-244/Domain: serine acetyltransferase homology <SAT>

RESULT 11  
 S29568

Query Match 39.5%; Score 648.5; DB 2; Length 273;  
 Best Local Similarity 51.2%; Pred. No. 2e-46; Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;  
 C; Species: Salmonella typhimurium  
 C; Date: 22-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-May-2000  
 C; Accession: S29568  
 R; Srivaprabad, A.V.; Kuczek, E.S.; Bawden, C.S.; Rogers, G.E.  
 A; Submitted to the EMBL Data library, May 1991  
 A; Reference number: S29567  
 A; Accession: S29568  
 A; Molecule type: DNA  
 A; Residues: 1-273 <SIV>  
 A; Cross-references: EMBL:X59594; NID:947659; PIDN:CAA42163.1; PID:gi47660  
 C; Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C; Keywords: acyltransferase; coenzyme A  
 F; 84-244/Domain: serine acetyltransferase homology <SAT>

Query Match 39.5%; Score 648.5; DB 2; Length 273;  
 Best Local Similarity 51.2%; Pred. No. 2e-46; Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;  
 C; Species: Salmonella typhimurium  
 C; Date: 22-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-May-2000  
 C; Accession: S29568  
 R; Srivaprabad, A.V.; Kuczek, E.S.; Bawden, C.S.; Rogers, G.E.  
 A; Submitted to the EMBL Data library, May 1991  
 A; Reference number: S29567  
 A; Accession: S29568  
 A; Molecule type: DNA  
 A; Residues: 1-273 <SIV>  
 A; Cross-references: EMBL:X59594; NID:947659; PIDN:CAA42163.1; PID:gi47660  
 C; Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C; Keywords: acyltransferase; coenzyme A  
 F; 84-244/Domain: serine acetyltransferase homology <SAT>

RESULT 13  
 G82049

Query Match 39.5%; Score 648.5; DB 2; Length 273;  
 Best Local Similarity 51.2%; Pred. No. 2e-46; Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;  
 C; Species: Vibrio cholerae  
 C; Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 C; Accession: G82049  
 C; Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clinton, R.A.; Gwinn, M.L.; Dodson, R.R.;  
 chardson, D.; Erauiaea, M.D.; Yamane, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers  
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